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KKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYE

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HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQILDGVNYLHT

PLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFI

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Best Local Similarity 9
Matches 260; Conservati
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R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR002245; Tyr kinase.

R InterPro; IPR001245; Tyr kinase.

Pfam; pF000169; pkinase; 1.

PROSITE; pS00107; PROTEIN_KINASE_DOW; 1.

R PROSITE; PS00101; PROTEIN_KINASE_DOW; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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-!- SIMILARITY: BELONGS TO EMBL; AB018001; BAA88063.1 HSSP; Q63450; 1A06.
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01-MAY-2000 (TrEMBLrel. 1
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Kawai T., Nomura F., Hoshino K., Copeland
Jenkins N.A., Akira S.;
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Pred. No. 1.1e-94;
1; Mismatches 2
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apoptosis through its cat
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Best Local Similarity
Matches 256; Conser
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MGD; MGI:1341297; Dapk2.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1
PRINTS; PR00109; TYRKINASE.
SMART; SM00220; STKC; 1
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1
PROSITE; PS00108; PROTEIN_KINASE_ST; 1
PROSITE; PS00108; PROTEIN_KINASE_ST; 1
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Q9QYM4;
01-MAY-2000
01-MAY-2000
01-DEC-2001
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SEQUENCE 3
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Kawai T., Nomura F., Hoshino K., Copeland N.G.,
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Mammalia; Eutheria;
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KINASE 2.
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Pred. No. 7.7e
2; Mismatches
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